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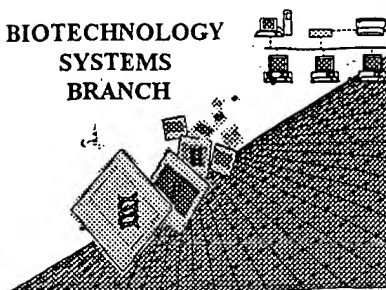
BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/701,926_

Source: _PCT/09_   **BEST AVAILABLE COPY**

Date Processed by STIC: _10/26/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/701,926

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF1

1 ____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
        Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

2 ____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
        Numbering   use space characters, instead.

4 ____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                   ensure your subsequent submission is saved in ASCII text.

5 ____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                         each n or Xaa can only represent a single residue. Please present the maximum number of each
                         residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
        "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                     Artificial or Unknown sequences.

7 ____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                           (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           This sequence is intentionally skipped

                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
        (NEW RULES)   <210> sequence id number
                           <400> sequence id number
                           000

9 ____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                             In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
        Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                        is Artificial Sequence

11 ____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                       Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                       "Unknown." Please explain source of genetic material in <220> to <223> section.
                       (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
        "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
                      any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT09

RAW SEQUENCE LISTING   DATE: 10/26/2001
PATENT APPLICATION: US/09/701,926   TIME: 16:12:56

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Output Set: N:\CRF3\10262001\I701926.raw

Does Not Comply
Corrected Diskette Needed

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10 <141> CURRENT FILING DATE: 2000-12-04
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ERRORED SEQUENCES

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PATENT APPLICATION: US/09/701,926   TIME: 16:12:56

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RAW SEQUENCE LISTING   DATE: 10/26/2001
PATENT APPLICATION: US/09/701,926   TIME: 16:12:56

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    331 gtgatgctga aattatagga attcgttaca tcagtgtaga ttccgaacac agtctgtgtg 360
    332 gtcttatgtg ttttgtaact tcttgcagca aaaggctaat gtgttttata ctataaatac 420
    333 aagtcaagtt tgattgaacc acaaacaagg ctcattgtat ctgtatattg cacgcgaaag 480
```

RAW SEQUENCE LISTING   DATE: 10/26/2001
PATENT APPLICATION: US/09/701,926   TIME: 16:12:56

Input Set : A:\SequenceListing.txt
Output Set: N:\CRF3\10262001\I701926.raw

```
    334 tggctagtgt atatagtatt gtcttatatc cgtcatcttg gaggaagaaa atcgtgtcct 540
    335 cagttttctg atattctgct catcaatcat cgactagcca atacactttg gccctacata 600
    336 tacacatact tatgagaagg aaaatacgaa atacgctcct tcaagacgag ttgaactttg 660
    337 taaattgttg tagtattagt atatgttaat gaggaaatgt agattttgtt gtagtttggt 720
    338 gatttgtaga atctgtctta taaagggact tacatgttga ggcaaactgt ataaaggtta 780
    339 aattgtcaat aacacacatc aaaatattgg accagtattt taagtaattt tttctgtata 840
    340 aaggctatgt tgctcaaatc cttcaaaaat ctcgacagat gcatggcacc ggtagtgcat 900
    341 tttttttgaat gagctggata cgagtgcaat aatatatttg ggaagtttga gcaaaataga 960
    342 cctgaaatta cttttagctt ttcttttttta aaggaatcgg atatgggtac aataatattt 1020
    343 ttgaagagtc tgagcaacat agactactct cggtaggatg aggataagat tgaaatttta 1080
E--> 344 aaatgctcta aagagaaaat ttgtggataa gattctccac taatttttnt atgacatgat 1140
    345 gagattctgc ctaagagttc caagaatatg gtgcacctgt taataatgta tatattataa 1200
    346 tagcataatc cactgttatg atttttagcaa gctcctttttt gtaatatatg aatgaacata 1260
    347 aaatataaaaa aggagagtta tatttgaacc atataaaaaa tgttacaagt atttttatat 1320
    348 gaataatata ataaaaagta aacctttttcg acaaaaaatt gattcatttc ccttttttaac 1380
    349 aattataacg gttttttaaat cctaatatac acctagtaaa aatatctatt tcaacccttc 1440
    350 tcgcagctgt attgcctaaa acccatatca cccccacgta gcctaaaatt tactttatac 1500
    351 tacgttgttt tgtttctcat ttttatttat ctttaattta tatcctgtaa aaagactcaa 1560
    352 agatgttttc tttaaatttt actttatttt ttttaggata aaaaatttgc aattcctaa  1619
    354 <210> SEQ ID NO: 13
    355 <211> LENGTH: 1193
    356 <212> TYPE: DNA
    357 <213> ORGANISM: Tomato
    359 <400> SEQUENCE: 13
    360 tgagtagaag ataaacttga caacgcatta gctcgaataa gagcataaat aaaaaagttt 60
    361 taactttaag aatccgtgca aaaaatcatc tactcaatta actcgatcaa tattctttca 120
    362 tcggtaactt acccgtttgg tattatatgt gtaaatatac ctaaatataa atacgagtct 180
    363 ataataacct aataaaaata ttaggcataa tagcggtgtt gttttgttag actcagtatt 240
    364 tttttatattt tataaaataa atactacgct ctttcaccaa acaattcttc aacgttaaat 300
    365 attcttgacg gtttttgttct gaaactatga ttctctttta gattttggtt ttgttgattt 360
    366 ctgatcaaaa actaaaagag aataattctt ctcccatttt attgctatct ttttatgatt 420
    367 gatttgttgg gggttcagca aatttatttta tgttctttta gtttttcctc ttttatctgt 480
    368 atttgaatct tgatcaatta atgttctttg atcatttgtt tgttagaatc caaatacgcg 540
    369 agcaagagaa aaagatttag gaaatgagta aagattggat ttttatggga aagatctaaa 600
    370 gatttggttg aagggattaa tgaattgagc atatgagcta aaaaatcaat cttggtgagt 660
    371 agggtatgtt atttgtggaa gttttgttag cttttcttgt atgtattgat attagatgat 720
E--> 372 ttaaacagag tcactaacat tcatatagct gaccttgaat tgtttaggnc agtggcgtag 780
    373 tagttgttgt tgttataaga gaatgagtgc tatggggagg ataggtagtt acataggtag 840
E--> 374 aggggtacgt agtgtttcgg ggacgttgaa tccatttggt ggtnctgtgg atatcattgt 900
    375 ggtgaggcag ccagatggga gtttgaaatc aactccttgg tatgttagat ttgggaagat 960
    376 tcaggggggtt ttgaaggcta gagaaaatgc ggttaatgta agtgtcaatg gcgttgaagc 1020
    377 tggtttttcgt atgaatttag atactagagg gcaggcatac ttcctaaggg agcgagacat 1080
    378 ggaaaatgga tattctttaa ctactcgaac atttgaacaa cttgcacctt tgaatctgaa 1140
E--> 379 ggaggaaaga atgtggttga ttcncctgct caaaacccca gcccgggccg tcg       1193
    381 <210> SEQ ID NO: 14
    382 <211> LENGTH: 222
    383 <212> TYPE: DNA
    384 <213> ORGANISM: Tomato
    386 <400> SEQUENCE: 14
```

```
              RAW SEQUENCE LISTING              DATE: 10/26/2001
              PATENT APPLICATION:  US/09/701,926   TIME: 16:12:56

                 Input Set : A:\SequenceListing.txt
                 Output Set: N:\CRF3\10262001\I701926.raw
```

```
E--> 387 tatgttgctc aaatccttca aaaatctcga cagatgcatg nnnnnnnnng cacccggtag 60
     388 tgcatttttt tgaatgagct ggatacgagt gcaataatat atttgggaag tttgagcaaa 120
E--> 389 atagacctga aattactttt agcttttctt ttttaaagnn nnnnnnnnnn nngaatcgga 180
E--> 390 tatgggtaca ataatatttt tgaagagtcn tgagcaacat ag            222
     392 <210> SEQ ID NO: 15
     393 <211> LENGTH: 222
     394 <212> TYPE: DNA
     395 <213> ORGANISM: Potato
     397 <400> SEQUENCE: 15
     398 tatgttgctc aaacacttca aaaatgtcca caggtgcgtg tcggatactc caaaaagtag 60
E--> 399 tgtatttagg tgtgtgnnnn tgatattagt nnnagtgtat atttaggntg tgtgtggata 120
E--> 400 gtagnnntgt atttagatgt gtgtgatatt tcaaaaagtt gtgtattttg gagaatttga 180
     401 tacgggtgcg gcaacaattt tgaagagtca ggagcaaaat ag            222
     531 <210> SEQ ID NO: 32
     532 <211> LENGTH: 1588
     533 <212> TYPE: DNA
     534 <213> ORGANISM: Tomato
     536 <400> SEQUENCE: 32
     537 atcaagttga aatatgttaa caaaatgtac agtttattta ttttttatttt atttataaaa 60
     538 aaaaaattgt acaaagaaac aaaatcccct ccttctgtat ttccatgtga tgtttaaatg 120
     539 gcatttgagt aaaagccaca aaaggcccat gtgaaattta taaaattttg aaacatttt 180
     540 gcataacaaa acaatacata agaggacacg taaaacttac taaaagagtt tttagttacg 240
     541 tataagcaaa gtttgagatt cccaagaaga aagagtttga aaatactaaa tgtcttgttg 300
     542 tcatccatat atatatatat gaatgaattc tcacatttgt gatcaagatt tctttatgca 360
E--> 543 tgntaatatt tatatttgga aattaaccgt cgattaatta agattatcat tgaataaggt 420
     544 ttgaaaaaga taaattgaac tatttcactt ttggagtgtt attgttatct gctaggtcaa 480
     545 tttagaatca taaattggaa ataaaaagac aacaatgccc tttttctttc ttggatactt 540
     546 tgaggttgta ctaaaggaca tataaaaagg tgaaaaagct aaaagtttca ctaataacta 600
     547 attttttattt tactttgtct tgtgtactaa acttttccat gtcttttcct ttcaatttcc 660
     548 agttgtgatg gatagtaaat tttctatagc attcaacaca aggacaaaac actaagcaac 720
     549 aaaagcatcc aaaaaccaag attagcaatg tgcaaatgaa gctttatgta tgatcaaaaa 780
     550 cacaacttgg aagttggaac tacctatctt agattccatc actttttttt tgttctccat 840
     551 cgatattcat cgatattcag tattcgagct ccgattaaat cataattcga taaagcgtac 900
     552 tttaataaaa ataatttcac tcgaaggctt caatctgaaa ccactgatta ttaaaaatga 960
     553 aagaattcta tcattattcc atatcttttt aggagattca agttaaaata gacaaccttt 1020
     554 ttctttaaat attgtcacaa tggtaataga tgcatgcgcg cctaatttca catttttaa 1080
     555 tataccaggc tatcattaac tttttttta tttaaaaaac tttaatgatt tcgaagaaat 1140
     556 aatgactata taaaaaaaac aagaaatatt agtagccatc attatgtata tgagcaaaca 1200
     557 aaacgaaaat ggaactatgg caacatcatg gaagctagga ataaacagct ccacttcaca 1260
     558 agagaacaaa gttcatgttg tactattata cctttttta ttttgacctc ttttaatatc 1320
     559 gtatatatta agcaagttgt taatcatata ccatcttta aatatttact tttgaaatca 1380
     560 taaaaaaatt gatgaaaaaa gttattatca tatctgttct tgcgtgagaa ataacaaata 1440
     561 tatttaagat gcacaaaaat tgattcgaac tagactttt ttaaaaaaaa ataaaaaaca 1500
     562 tgatgaaact ctaggtgggg tattctttt gtcaattact actaacaaag attgttgaaa 1560
     563 aagaagccaa ttatatgatt catcaata            1588
     565 <210> SEQ ID NO: 33
     566 <211> LENGTH: 1307
     567 <212> TYPE: DNA
     568 <213> ORGANISM: Tomato
```

```
      570 <400> SEQUENCE: 33
      571 ttggacttcc tacccagcag ttcacacatc aatatcattt aattaaaatt aaagccattt 60
      572 atttaggaaa taaatagcat aaaaaaaaca ctaataatta aaacatttgt gtcaaaggga 120
      573 aagtatattg actaattttt tgcatatgtg gttcaaagga ggaatttttt aattacaaaa 180
      574 aaaaaagttt tatggtggga atcaaacata ttataggata attaaagaga tggatttatt 240
      575 atattttgtg taatctatta attattaaat ggcttaattt tgtatccact aataatataa 300
      576 gtaatttcta tatattcagt acaatttgac tagctccaac agctttccca gtaacacata 360
      577 tttatacagt tgcatctcac tataataaaa atatgtaaat attttctctt taccgtaact 420
      578 ccagtaaaac ttaaactcta attaataata caacactaat ctaggcaagc tgtagactgt 480
      579 aattaattgc atgttttaaa tctgtgaagg gtcgtttggc ataaaaatac ataatgcagg 540
      580 gattattaac gtatagatta gtaatacata gattagtaat gcatggatta gttttttatca 600
      581 agtgtttgat tcattgtttc ctacttaatc ttatgtttag tttaaaactc tagaaaaata 660
      582 tatttcctat tataccttg agttattgtg agaatttgta tttcatttaa ctagtcaagt 720
E--> 583 taaatncnaa tttatatata tatatatata ttattaattt tgaggtgtga tatgtcacac 780
      584 tgtatatttt taatttttttg ttggtcaaat ataccttgaa cttaaacatg gatttaaggc 840
E--> 585 tatttaaatt gttcaaatac acgaacctta tttttttttat aaaanaatca agtggtcaat 900
E--> 586 cgcaaactac atttataaaa naaaggccaa aaaaatcaat ccaatataac agctcataca 960
      587 tggagaaaaa attagtttat gaaatcatca aattacatgg aataaatttg gagaatttaa 1020
E--> 588 atgaatattt ataaatattt tcatataaat aaaaaagaac attaattaca aatanaataa 1080
      589 tagaaaaaaa atttgaggat attttagtca ttttggaatc ttttcgaagg attgctaaac 1140
      590 cttgaattag ctatccctcc atttcctagg gataaaataa gaccttgtat gaggtataac 1200
      591 taatctatgg attaggttaa ataaagtaac caaacaatat ttttgttgga ctaaatttta 1260
E--> 592 atccatggat tcnttggatt aatacctcct accagcccgg gccgtcg 1307
      594 <210> SEQ ID NO: 34
      595 <211> LENGTH: 255
      596 <212> TYPE: DNA
      597 <213> ORGANISM: Tomato
      599 <400> SEQUENCE: 34
      600 ggtcgtttgg cataaaaata cataatgcag ggattattaa cgtatagatt agtaatacat 60
      601 agattagtaa tgcatggatt agtttttatc aagtgtttga ttcattgttt cctacttaat 120
E--> 602 cttatgttta gtttaaaact ctagaaaaat anntatttcc tattatacct ttgagttatt 180
E--> 603 gtgagaattt gtatttcatt taactnagtc aagttaaatn cnaatttata tatatatata 240
      604 tatattatta atttt 255
      606 <210> SEQ ID NO: 35
      607 <211> LENGTH: 255
      608 <212> TYPE: DNA
      609 <213> ORGANISM: Tomato
      611 <400> SEQUENCE: 35
E--> 612 gatcgtacgg tacaaagatc aatacttcag gnnnnnnnnn nnnnnngagt agtaatacat 60
E--> 613 tttttggtaa tgcagagatt antttttatc aagtgtttgg ttcattgttt nttacctaat 120
      614 tttgtgtgtg gtttaaagtt tacaaaaaat aattctttcc aattatacgc taaagttatt 180
E--> 615 atgagatttt atatttcatg taattgggtc aannnaatag ataattgacc gataatatta 240
      616 ttttttataa cattt 255
      647 <210> SEQ ID NO: 39
      648 <211> LENGTH: 197
      649 <212> TYPE: DNA
      650 <213> ORGANISM: Tomato
      652 <400> SEQUENCE: 39
E--> 653 ttatatattt gtatttgtat aaagtgaaag agacgatgnn gagagtagcg agcgagatta 60
```

```
E--> 654 aaaaagagtg gcgaacgnnn nnagatatgc cgtaaattag aattaaatga aactgtcatt 120
E--> 655 ataacattta ttttgaataa ataattttga tataatacac aattttcnnt taaaaagcaa 180
E--> 656 cgannnnnng ataatgt                                              197
```

item 9

VERIFICATION SUMMARY   DATE: 10/26/2001
PATENT APPLICATION: US/09/701,926   TIME: 16:12:57

Input Set : **A:\SequenceListing.txt**
Output Set: **N:\CRF3\10262001\I701926.raw**

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:136 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:200 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:285 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:314 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:326 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
M:340 Repeated in SeqNo=12
L:372 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:387 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:399 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:543 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:583 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
M:340 Repeated in SeqNo=33
L:602 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:612 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:653 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39